

## **FIGURE 1**

GGACTAATCTGTGGGAGCAGTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT  
GTTGAAGGGTGTCCCCCTTAAATGTAATACCTCCTCATCTTCTTACACAGTG  
TCTGAGAACATTACATTAGATAAGTAGTACATGGTGGATAACTCTACTTTAGGAGGA  
CTACTCTTCTGACAGTCCTAGACTGGTCTCTACACTAAGACACCATGAAGGAGTATGTG  
CTCCTATTATTCCCTGGCTTGTGCTGCAAACCCCTTTAGCCCTCACACATCGCACT  
GAAGAACATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATG  
ATGATGATGATGAGGACAACCTCTTTCCAACAAGAGAGCCAAGAAGCCATTTTCCA  
TTTGATCTGTTCCAATGTGTCATTGGATGTCAGTGCTATTCAAGGAGTTGACATTGCTC  
AGATTTAGGTTGACCTCAGTCCAAACACATTGATACTCGAATGCTGATCTTC  
AAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTAAAGGACTCACTTCACTTATGGT  
CTGATCCTGAACAACAACAGCTAACGAAGATTCAACCCAAAGCCTTCTAACACAAAGAA  
GTTGCGAAGGCTGTATCTGTCACATCAACTAAGTGAATACCACTTAATCTCCAAAT  
CATTAGCAGAACTCAGAATTGAAATAAAGTTAAGAAAATACAAAGACACATTCAA  
GGAATGAATGCTTACACGTTGGAAATGAGTGCAAACCCCTTGTATAATAATGGGATAGA  
GCCAGGGGCATTGAAGGGGTGACGGTGTCCATATCAGAATTGCAAGCAGAAACTGACCT  
CAGTTCTAAAGGCTTACCAACTTATTGGAGCTTCACTTAGATTATAATAAAATTCA  
ACAGTGGAACTTGAGGATTTAAACGATACAAAGAACTACAAAGGCTGGCCTAGGAAACAA  
CAAATCACAGATATCGAAAATGGGAGTCTGCTAACATACCACGTGTGAGAGAAATACATT  
TGGAAAACAATAAACTAAAAAAATCCCTCAGGATTACCAAGAGTTGAAATACCTCCAGATA  
ATCTTCCTTCATTCTAATTCAATTGCAAGAGTGGAGTAATGACTCTGTCCAACAGTGCC  
AAAGATGAAGAAATCTTATACAGTGCAATAAGTTATTCAACAACCGGTGAAATACTGGG  
AAATGCAACCTGCAACATTGTTGTGTTGAGCAGAATGAGTGTAGCTGGAAACTTT  
GGAATGTAATAATTAGTAATTGGAATGTCCTTAAATATAAGATTCAAAATCCCTACATT  
TGGAAATCTGAACTCTATTAAATAATGGTAGTATTATATAACAGCAAATATCTATTCTCA  
AGTGGTAAGTCCACTGACTTATTGACAAGAAATTCAACGGAATTTCGCCAACTATT  
GATACATAAGGGGTGAGAGAAACAAGCATCTATTGCAAGTGGCTTGTGCTACAAATGAT  
CTTACATAAAATCTCATGCTTGACCATTCCTTCTTCATAACAAAAAGTAAGATATTGGTA  
TTAACACTTGTATCAAGCACATTAAAAGAACTGTACTGTAATGGAATGCTGACT  
TAGCAAATTGCTCTTCTTGCTGTTAGAAAAACAGAATTAAACAAAGACAGTAATGT  
GAAGAGTGCATTACACTATTCTTATTCTTAGTAACGGTAGTACTGTAATATTAAAT  
CATCTAAAGTATGATTGATATAATCTTATTGAAATTACCTTATCATGCTTAGAGCCGT  
CTTATGTTAAAACAATTCTTAAAATAAGCCTTCAGTAAATGTCATTACCAACTTGA  
TAAATGCTACTCATAAGAGCTGGTTGGGCTATAGCATATGCTTTTTTTTAATTATT  
ACCTGATTAAAATCTGTAAAACGTGTAGTGTTCATAAAACTGTAACCGCATT  
AATGATCCGCTATTATAAGCTTTAATAGCATGAAATTGTTAGGCTATATAACATTGCCAC  
TTCAACTCTAAGGAATATTGAGATATCCCTTGGAAAGACCTGCTGGAAAGAGCCTGGA  
CACTAACAAATTCTACACCAAATTGCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA  
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAAACAGACAGAAACGAAAGCTCTA  
TATAAATGCTCAGAGTTCTTATGTATTCTTATTGGCATTCAACATATGAAAATCAGAAA  
ACAGGGAAATTTCATTAAAATATTGGTTGAAAT

## **FIGURE 2**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392
<subunit 1 of 1, 379 aa, 1 stop
<MW: 43302, pI: 7.30, NX(S/T) : 1
MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDEDNSLFPTREPR
SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNNKLTKIHPKAFLTTKLRRLYLSHNQLSEIPLNLPKSLAELRIHENVKKIQ
KDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNNKITDIENSLANIPRVREIHLENNKLKKIPSGLPEL
KYLQIIIFLHSNSIARGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV
QLGNFGM
```

**Signal sequence.**

amino acids 1-15

**N-glycosylation site.**

amino acids 281-285

**N-myristoylation sites.**

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

**Leucine zipper pattern.**

amino acids 154-176

### **FIGURE 3**

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## **FIGURE 4**

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLGLLLGSRPARGAGPEPPVLPIRSEKEPLPVRAAGCTFGGKVYALDE  
TWHPDLGQPGVMRCVLCACEAPQWGRTRGPGRVSKNIKPECPTPACGQPRQLPGHCCQT  
CPQERSSSERQPSGLSFEYPRDPEHRSYSDRGEPGAERARGDHTDFVALLTGPRSQAVER  
ARVSLLRSSLRFSISYRRLDRPTRIRFSDSNGSVLFEHPAAPTQDGLVCGVWRRAVPRLSLRL  
LRAEQLHVALVTLTHPSGEVGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTLSDTED  
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGQLLRELQANVSAQEPGFAEVLPNLTQEMD  
WLVLGELQMALEWAGRPLRISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN  
GSLIYQVQVVGTSSEVVAMTLETKPQRRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML  
LQNELFLNVGTKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVKSQAAGHAWLS  
LDTHCHLHYEVLLAGLGGSEQGTVTAHLLGPPGTPGPRRLKGFYGSEAQGVVKDLEPELLR  
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGLRLEAAGAEGVRALGAPDTASAAPPVV  
PGLPALAPAKPGGPGRPRDPNTCFEGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVCP  
PPSCPHVQAPDQCCPVCPEKQDVRDLPGLPRS RDGEGCYFDGDRSWRAAGTRWHPVVPPF  
GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPVRVNPTDCCKQCPVGSGAHPQLGDPMQADG  
PRGCRFAGQWFPEQSWSHPSVPPFGEMSCITCRCGAGVPHCERDDCSLPLSCSGKESRCCS  
RCTAHRRPPETRTDPELEKEAEGS

**Signal sequence.**

amino acids 1-23

**N-glycosylation sites.**

amino acids 217-221, 351-355, 365-369, 434-438

**Tyrosine kinase phosphorylation sites.**

amino acids 145-153, 778-786

**N-myristylation sites.**

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,  
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,  
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,  
905-911

**Amidation site.**

amino acids 87-91

**Cell attachment sequence.**

amino acids 165-168

**Leucine zipper pattern.**

amino acids 315-337

## **FIGURE 5**

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGGCCACTGCCACCGCCGCCGCGCAGCTGC  
TCCTGGCTCCGGCTCCCGGCCCTCCCGGCCGGCATGCAGCCCCGCCGCGCCCAGGCGCCGGTGCAGCTGC  
TGCCTGGCGCTGGCCCTGCTGCTGCTGCTGGAGCGGGGCCCCGAGGCAGCTCCCTGGCCAACCCGGTGCCCG  
CCGGCCCTTGTCTGCGCCCCGGCGTGCCTGGCAGGCCCTGCCGAATGGGGGTGTGTCACCTCGCGCCCTG  
AGCCGGACCGCAGCACCCGGCCCCGGCGAGCCTGGTACAGCTGACCTGCCGGATCTCCGGCG  
CCAAGTGCAGCTGTCAGATCCTGTGCCAGCAACCTTGTACCATGGCAACTGCAGCAGCAGCAGCA  
GCAGCAGCGATGGCTACCTCTGCAATTGCAATGAAGGCTATGAAGGTCCAACGTGAACAGGCACTCCAGTC  
TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCGACAGCTTCAGCCTGTTCTGACTCAGGAGCCTGACA  
AAATCCTGCTCGCTCTCAGGCAACGGTACACTGCCTACCTGGCAGCGAAAACAGGGCAGAAAGTTGTAGAAA  
TGAAATGGGATCAAGTGGAGGTGATCCCAGATATTGCTGTGGGAATGCCAGTTCAACAGCTCTGGGGTGGCC  
GCCTGGTATCCTTGAAGTGCACAGAACACCTCAGTCAGATTGCCAGATGCCACTGCCACTGATTG  
TCTGGAAGGTACGGCCACAGGATTCCAACAGTGCCTCCATAGATGGACGAAGTGTGACCCCCCTCAGGCTT  
CAGGGGGACTGGTCTCTGGAGGAGATGCTGCCCTGGGAATAATCACTTTATTGGTTTGTGAATGATTCTG  
TGACTAAGTCTATTGTGGCTTGCCTTAACCTGGTGGTGAAGGTACGCACCTGTGTGCCGGGGAGAGTCAGC  
CAAATGACTTGGAGTGTTCAGGAAAAGGAAAATGCACCAAGCGTCAGAGGCAACTTTTCTGTACCTGTG  
AGGAGCAGTACGTGGTACTTCTGTGAAGAATACGATGCCAGAGGAAACCTGCCAAAACAACCGCAGC  
GTATTGATGCAAATGAAAAGCAAGATGGAGCAATTACCTGTGTGTTGCCCTGGTTACTGGAGAGCTT  
GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTCCAGTCTCAGTGGAT  
TCACCTGCCAGTGTCCAGAAGGATACTCGGATCTGCTGTGAAGAAAAGGTGGACCCCTGCGCCTCGTCTCCGT  
GCCAGAACACGGCACCTGCTATGTGGACGGGTACACTTACCTGCAACTGCAGCCGGCTTCACAGGGCGA  
CCTGTGCCAGCTTATTGACTCTGTGCCCTCAGCCCTGCTCATGGCACGTGCCAGCGTGGGACCAGCT  
ACAAATGCCCTGTGATCCAGGTTACCATGCCCTACTGTGAGGAGGAATAATGAGTGCCTCTCGCTCCAT  
GCCCTGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGTGCCCTGGCAGAAATCAAAGGAACAC  
ACTGTGAATTGTACAAGGATCCCTGCGCTAACGTCAGCTGTGAACGGAGCCACCTGTGACAGCAGGCCCTGA  
ATGGCACGTGCATCTGTGCAACCAGGTTACAGGTGAAGAGTGCACATTGACATAATGAATGTGACAGTAACC  
CCTGCCACCATGGGGAGCTGCCCTGACCAGCCAATGGTTATAACTGCCACTGCCCATGGTTGGGGAG  
CAAACGTGAGATCCACCTCAATGGAAGTCCGGCACATGGCGAGAGCCTACCAACATGCCACGGCACTCCC  
TCTACATCATCATTGGAGCCCTGCGTGGCCTCATCCTTATGCTGATCATCCTGATCGTGGGATTGCCGCA  
TCAGCCGATTGAATACCAGGGTTCTCCAGGCCAGCCTATGAGGAGTCTACAACGCCAGCATGACAGCG  
AGTTCAAGCAATGCCATTGCAATCCATCGGCATGCCAGGTTGGAAAGAAATCCCGGCTGCAATGTATGATGTGA  
GCCCATGCCCTATGAAGATTACAGTCTGATGACAAACCCCTGGTACACTGATTAAAACCTAAAGATTGTAAT  
CTTTTTGGATTATTTCAAAAGATGAGATACTACACTCATTTAAATATTTAAGAAAATAAAAGCTTAA  
GAAATTAAAATGCTAGTGTCTCAAGAGTTTCACTGAGAATATTAAGAACTAATTCTGCACTGTTAGTTG  
AAAAAAATTTAAAAACAAATTGTGAAACCTATAGACGATGTTTAATGTACCTTCAGCTCTAAACTGT  
GTGCTTCTACTAGTGTGTCTTTCACTGTAGACACTATCACGAGACCCAGATTAATTCTGTGGTTGTTACA  
GAATAAGTCTAATCAAGGAGAAGTTCTGTTGACGTTGAGTGCCGCTTCTGAGTAGAGTTAGGAAAACCAC  
GTAACGTAGCATATGATGTATAATAGAGTATAACCGTTACTTAAAGAAAGTCTGAAATGTTGTTGTGAAA  
AGAAACTAGTTAAATTACTATTCTAACCGGAATGAAATTAGCCTTGCTTATTCTGTCATGGTAAGTAA  
TTATTCTGCACTGTTGTGAACTTGTGAAACATTCTTCGAGTTGTTTGTCACTTCTGTAACAGTC  
TCGAACTAGGCCTCAAAACATACGTAACGAAAAGGCCAGCGAGGCAAATTCTGATTGATTGAATCTATATT  
TTCTTAAAGTCAAGGGTTCTATATTGTGAGTAAATTAAATTACATTGAGTTGTTGTTGCTAAGAGGTAG  
TAAATGTAAGAGAGTACTGGTCCCTCAGTAGTGTAGTATTCTCATAGTGCAGCTTATTATCTCAGGATGTT  
TTTGTGGCTGTATTGATTGATATGTGCTTCTGATTCTGCTAATTCCAACCATATTGAATAATGTGATC  
AAGTCA

## **FIGURE 6**

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLL GAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR  
PEPDHQHPAPAGEPGYSCTCPAGISGANCQLVADPCASNPCHGNCSSSSSSDGYLCICN  
EGYEGPNCEQALPSLPATGWTEMAPRQLQPVPATQEPDKILPRSQATVTLPTWQPKTGQKV  
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQ  
QCSLIDGRSVTPLQASGGLVLLEEMLALGNNHFIGFVNDSVTKSIVALRLTLVVKVSTCVPG  
ESHANDLECSGKGKCTTKPSEATFSCTCEEQYVGTCEEYDACQRKPCQNNASCIDANEKQD  
GSNFTCVCLPGYTGELCQSKIDYCILDPCRNGATCISSLSGFTCQCPEGYFGSACEEKVDPC  
ASSPCQNNGTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCSRSGTSYKCLCDPG  
YHGLYCEEYNECLSAPCLNAATCRDLVNGYECVCLAEYKGTHCELYKDPCANVSLNGATC  
DSDGLNGTCICAPGFTGEEDIDINECDSNPCHGGSCLDQPNGYNCHCPHGWVGANCEIHL  
QWKSGHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYN  
CRSIDSEFSNAIASIRHARFGKKSRAAMYDVSPIAYEDYSPDDKPLVTLIKTKDL

**Signal sequence.**

amino acids 1-28

**Transmembrane domain.**

amino acids 641-660

**N-glycosylation sites.**

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,  
375-379, 442-446, 549-553, 564-568

**Glycosaminoglycan attachment site.**

amino acids 320-324

**Tyrosine kinase phosphorylation sites.**

amino acids 490-498, 674-682

**N-myristoylation sites.**

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,  
373-379, 449-455, 480-486, 562-568, 565-571

**Amidation site.**

amino acids 702-706

**Aspartic acid and asparagine hydroxylation site.**

amino acids 520-532, 596-608

**EGF-like domain cysteine pattern signatures.**

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,  
491-503, 529-541, 567-579, 605-617

## **FIGURE 7**

CTCTGGAAGGTACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTCAGGCTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTGGGAATA  
ATCACTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCCTTAAC  
CTGGTGGTGAAGGTACGCACCTGTGCGCCGGGGAGAGTCACGCAAATGACTGGAGTGTTC  
AGGAAAAGGAAAATGCACCAAGCCGTAGAGGCAACTTTCTGTACCTGTGAGGAGC  
AGTACGTGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAAACAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTACCTGTGTTGCCTTCC  
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGAG

## **FIGURE 8**

CTCTGGAAAGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTCAGGCTTCAGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTGGGAATA  
ATCACTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCGCTTAAC  
CTGGTGGTGAAGGTAGCACCTGTGTGCCGGGGAGAGTCACGCAAATGACTGGAGTGTTC  
AGGAAAAGGAAAATGCACCACGAAGCCGTAGAGGCAACTTTCTGTACCTGTGAGGAGC  
AGTACGTGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAACAAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGAGCAATTACCTGTGTTGCCTTCC  
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGGAG

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## **FIGURE 9**

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG  
GCCCCCCCAGAGCCCTCACCAACGCTGGCGCCCCAGAGCCCACACCATGCCGGCACCTAC  
GCTCCCTGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGCCCT  
GATGCGGGACTTCCCCTCGTGGACGGCCACAACGACCTGCCCCTGGTCTAAGGCAGGTTT  
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTCTAGCTACGCCAGACCAGCCTGGAC  
AGGCTTAGAGATGCCCTCGTGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA  
GGACCGGGATGCCCTCGCCTCACCCCTGGAGCAGATTGACCTCATACGCCATGTGTGCCT  
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC  
TGCCTCATCGGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT  
CTACATGCTGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCCTGGCAGAGA  
GCTCCGCTAAGGGCGTCCACTCCTCTACAACACATCAGGGCTGACTGACTTTGGTGAG  
AAGGTGGTGGCAGAAATGAACCGCCTGGCATGATGGTAGACTTATCCCATGTCTCAGATGC  
TGTGGCACGGCGGCCCTGGAAAGTGTACAGGCACCTGTGATCTTCTCCACTCGCTGCC  
GGGGTGTGCAACAGTGCCTCGGAATGTCAGGCTGATGACATCCTGCAGCTCTGAAGAAGAAC  
GGTGGCGTGTGATGGTGTCTTGTCCATGGGAGTAATAACAGTGCACCCATCAGCCAATGT  
GTCCACTGTGGCAGATCACTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGGA  
TTGGTGGAGATTATGATGGGCCGCAAATTCCCTCAGGGCTGGAAGACGTGTCCACATAC  
CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCC  
TCGTGGAAACCTGCTCGGGTCTTCAGACAAGTGGAAAGGTACAGGAAGAAAACAATGGC  
AAAGCCCCTGGAGGACAAGTCCCGATGAGCAGCTGAGCAGTTCCCTGCCACTCCGACCTC  
TCACGTCTCGCTCAGAGACAGAGTCTGACTTCAGGCCAGGAACACTCACTGAGATTCCCATA  
CTGGACAGCCAAGTTACCAAGGCCAGTGGTCAGTCTCAGAGTCCTCCCCCACATGCCAG  
TCCTTGCAGTTGTGGCACCTTCCAGTCCTTATTCTGTGGCTCTGATGATGACCCAGTTAGTCC  
TGCCAGATGTCAGTGTAGCAAGCCACAGACACCCACAAAGTCCCTGTTGTGCAGGCACA  
AATATTCTGAAATAATGTTGGACATAG

## **FIGURE 10**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595
<subunit 1 of 1, 433 aa, 1 stop
<MW: 47787, pI: 6.11, NX(S/T): 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRRCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAAEMNRLGMMVDSLHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAFFPVLIWL
```

**N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

**N-myristylation sites.**

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

**Renal dipeptidase active site.**

amino acids 134-157

## **FIGURE 11**

AAAACCTATAATATTCCGGATTATTCATACCGTCCCACCATGGGCGCGGATCCGCGGCCG  
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTGACCACACTCAGTAGTCCCAGCA  
CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCGCTCGTGGACGCCAC  
AACGACCTGCCCTGGTCTAAGGCAGGTTACCAGAAAGGGCTACAGGATGTTAACCTGCG  
CAATTTCAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGCGCCAGT  
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCTGGAG  
CAGATTGACCTCATGCCGATGTGCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC  
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC  
TGGACAATAGCCTCTCCATCTTACGTACCTCTACATGCTGGAGTGCCTACCTGACGCTC  
ACCCACACCTGCAACACACCCCTGGCAGAGAGCTCCGCTAAGGGGTCCACTCCTCTACAA  
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCTGGCA  
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG  
GCACCTGTGATCTTCTCCACTCGGCTGCCGGGGTGTGCAACAGTGCTCGGAATGTTCC  
TGATGACATCCTGCAGCTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTGTCCATGG  
GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC  
AAGGCTGTCATTGGATCCAAGTTCATCGGATTGGTGGAGATTATGATGGGCCGGCAAATT  
CCCTCAGGGGCTGGAAGACGTGTCCACATACCGGTCTGATAGAGGAGTTGCTGAGTCGTG  
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTCGTGGAAACCTGCTGCGGTCTTCAGACAA  
GTGGAAAAGGTACAGGAAGAAAACAATGGCAAAGCCCCTGGAGGACAAGTTCCGGATGA  
GCAGCTGAGCAGTCTGCCACTCCGACCTCTCACGTCTCGTCAGAGACAGAGTCTGACTT  
CAGGCCAGGAACTCACTGAGATTCCCACACTGGACAGCCAAGTTACCAGCCAAGTGGTCA  
GTCTCAGAGTCCTCCCCCACCCTGACAAAACCTCACACATGCCACCCTGCCAGCACCTGA  
ACTCCTGGGGGACCGTCAGTCTTCCCTTCCCCAAAACCCAAGGACACC

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## **FIGURE 12**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX (S/T) : 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRRMCAKYSELELVTSAKALND
TQKLAACLIGVEGGHSLDNSLSILRTFYMLGVRYLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLRSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHDKHTCPPCPAPELLGGP
SVFLFPPPKPKDT
```

095444270000

## FIGURE 13

CGCCCAGCGACGTGCGGGCGGCCTGGCCCGGCCCTCCCGCGCCCGGCCTGCGTCCC CGGCC  
CTGCGCCACCGCCGCCGAGCCGAGCCCGCGCCGGCAGCGCCGGCCCC **ATGCCC**  
GCCGGCCGCCGGGGCCCCGCCAATCCCGCGGCCGCCGGCAGCGCCGGCCCC  
GCTGCTGCTCTGCGTCCTCGGGGCCGAGCCGGATCAGGAGCCACACAGCTGTGATCA  
GTCCCCAGGATCCCACGCTCTCATCGGCTCCTCCCTGCTGCCACCTGCTCAGTGCACGGA  
GACCCACCAGGAGCCACCGCCGAGGGCCTCTACTGGACCCCTAACGGCGCCGCTGCC  
TGAGCTCTCCCGTGTACTCAACGCCTCCACCTGGCTCTGCCCTGGCCAACCTCAATGGG  
CCAGGCAGCGGTGGGGACAACCTCGTGTGCCACGCCGTGACGGCAGCATTGGCTGG  
TCCTGCCTCTATGTTGGCCTGCCAGAGAAACCGTCAACATCAGCTGCTGGTCCAAGAA  
CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCACGGGAGACCTCCACACCA  
ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGCCAGGACAACACATGTGAGGAGTAC  
ACAGTGGGCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGAT  
CTGGGTGGAGGCCACCAACCGCCTGGCTCTGCCGCTCCGATGTACTCACGCTGGATATCC  
TGGATGTGGTGACCACGGACCCCCCGCCGACGTGACGTGAGGCCGTGGGGCCTGGAG  
GACCAGCTGAGCGTGCCTGGGTGTCGCCACCCGCCCTCAAGGATTCCCTTTCAAGCAA  
ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGACGATGTGAGCA  
ACCAGACCTCCTGCCGCTGGCCGGCCTGAAACCCGGCACCGTGTACTCGTGCAGTGC  
TGCAACCCCTTGGCATCTATGGCTCCAAGAAAGCCGGATCTGGAGTGAGTGGAGCCACCC  
CACAGCCGCTCCACTCCCCGAGCTGAGGCCGGGCCGGCGGGCGGGCGTGCACCGC  
GGGCGGAGAGCCGAGCTGGGGCGGTGCGCGAGCTCAAGCAGTCCCTGGCTGGCT  
AAGAAGCACCGTACTGCTCCAACCTCAGCTCCGCTCTACGACCAGTGGCGAGCCTGGAT  
GCAGAAGTCGCACAAGACCCGAACCAGGACGAGGGATCCTGCCCTGGCAGACGGGCA  
CGCGAGAGGTCTGCCAGA**TAA**GCTGTAGGGCTCAGGCCACCCCTGCCACGTGGAGA  
CGCAGAGGCCGAACCAAACGGGCCACCTCTGTACCCCTACTCAGGGCACCTGAGCCAC  
CCTCAGCAGGAGCTGGGTGGCCCTGAGCTCCAACGCCATAACAGCTCTGACTCCACGT  
GAGGCCACCTTGGTGACCCAGTGGTGTGTGTGTGAGGGTTGGTTGAGTTGC  
CTAGAACCCCTGCCAGGGCTGGGGTGAGAAGGGAGTCATTACTCCCCATTACCTAGGGC  
CCTCCAAAAGAGTCCTTAAATAATGAGCTATTAGGTGCTGTGATTGTGAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAACAAAAAAA

0 1 2 3 4 5 6 7 8 9

## **FIGURE 14**

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSARRPPPLPLLLLCLVGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSV  
HGDPPGATAEGLYWTLN GRRLLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL  
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTGAHGETFLHTNYSLKYLRLWYGQDNTCEE  
YHTVGPHSCHIPKDLALFTP YEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVS RVGG  
LEDQLSVRWVSPPAKDFLFQAKYQIRYRVEDSVDKVVDDVSNQTSCRLAGLKPGTVYFVQ  
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSGPVRRELKQFLG  
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

**Signal sequence.**

amino acids 1-30

**Transmembrane domain.**

amino acids 44-61

**N-glycosylation sites.**

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 413-417

**N-myristoylation sites.**

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,  
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

**Amidation site.**

amino acids 3-7, 79-83, 411-415

**Growth factor and cytokines receptors family signature 2.**

amino acids 325-331

## **FIGURE 15**

CCACCGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTAGAGTGGTAAAAAA  
AAAAAAAAACACACCAACCGCTCGCAGCCACAAAAGGGATGAATTTCTTCTGGACATCCTC  
CTGCTTCTCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA  
GAGGAGAAAATCAGTCACCGGCAGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA  
GACTGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTTCTCTGGATATAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGTGCCAAGGTTACACCTTGT  
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGCACATTCTGGACTACAAA  
GGCATTCTCCTGCAATGACGAAGAATAACCATGCCATTGTCACTGTGGCTCGCAG  
CTGGACATGTCTCGTCCCTTACTGGCTTACTGTTCAAGCAAGTTGCTGCTGTTGGA  
TTTCATAAAACTTGACAGATGAACACTGGCTGCCTACAAATACTGGAGTCACAAACATG  
TCTGTGCTTAATTCGTAACACTGGCTCATCAAAATCCAAGTACAAGTTGGACCCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG  
ATTTTATTCCATCTCTATAGCTTTTAACAACATTGGAAAGGATCCTCCTGAGCGTT  
CCTGGCAGTTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAATAAGCACCTAGTTCTGAAAACGATTGACTTACCAAGGTTAGGTTGATGTCATCTA  
ATAGTGCCAGAATTAAATGTTGAACCTCTGTTCTAATTATCCCCATTCTCAATA  
TCATTGGAGGCTTGGCAGTCTCATTACTACCACCTGTTCTTAGCCAAAAGCTGATT  
ACATATGATATAACAGAGAAATACCTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA  
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTGCAA  
AATTGTACCATACCGTTATTAAACATATAATTGATTGATTGACTTAAATTGTTG  
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTAAATAAAA  
TGAAGGACTATCTAGTGGTATTTCACAATGAATATCATGAACCTCAATGGTAGGTT  
ATCCTACCCATTGCCACTCTGTTCTGAGAGATAACCTCACATTCAATGCCAACATTCT  
GCACAGGGAAGCTAGAGGTGGATACACGTGTGCAAGTATAAAAGCATCACTGGATTAAAG  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA  
AA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 16

```
</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436
<subunit 1 of 1, 300 aa, 1 stop
<MW: 32964, pi: 9.52, NX(S/T): 1
MKFLLDILLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDFLFTQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ
```

**Signal sequence.**

amino acids 1-19

**Transmembrane domain.**

amino acids 170-187

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 30-34, 283-287

**N-myristoylation sites.**

amino acids 43-49, 72-78, 122-128, 210-216

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## **FIGURE 17**

GAATGTTCTTGGAGTCTGGAGGAGGAAAGCGGAGCCGCAGGGAGCGAACCAAGGACTG  
GGGTGACGGCAGGGCAGGGGGCGCTGGCCGGGAGAAGCGCGGGGCTGGAGCACCAAA  
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATGGGGAGCCGGAGGGGGACT  
GCGAGAGGACCCCGCGTCCGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGC  
TGCTCCTGGCCTGGCGGCCGGCTGCCCGCCACTGGACGACAACAAGATCCCCAGCCTCTGC  
CCGGGGCACCCGGCCTCCAGGCACGCCGGCCACCATGGCAGCCAGGGCTGCCGGCG  
CGATGGCCGCGACGGCCGCGACGGCGGCCGGCTCCGGGAGAGAAAGGCAGGGCG  
GGCCGGACTGCCGGACCTCGAGGGACCCGGCCGCGAGGAGAGGCAGGGACCCGCGGG  
CCCACCGGGCTGCCGGGAGTGCTCGGTGCCTCCCGCATCCGCTTCAGCGCCAAGCGCTC  
CGAGAGCCGGTGCCTCCCGTCTGACGCACCCCTGCCCTGACCGCGTGGTGAACG  
AGCAGGGACATTACGACGCCGTACCGCAAGTTCACCTGCCAGGTGCCTGGGTCTACTAC  
TTCGCCGTCCATGCCACCGTCTACCGGCCAGCCTGCAGTTGATCTGGTGAAGAATGGCGA  
ATCCATTGCCCTTTCTTCAGTTTCGGGGGTGCCAAGCCAGCCTCGCTCTCGGG  
GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGTGCAGGTGGTGTGGTACTAC  
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTCTCCGGATTCTGGTACTCCGA  
CTGGCACAGCTCCCCAGTCTTGCTTAGTGCCACTGCAAAGTGAGCTATGCTCTCACTCC  
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTATCCAGGAGGGCTGGCCCCCTGGAATATT  
GTGAATGACTAGGGAGGTGGGTAGAGCACTCTCCGTCTGCTGGCAAGGAATGGAAC  
AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGCAGTGGCTGGATTCTGCCAAGACCA  
GAGGAGTGTGCTGTGCTGGCAAGTGTAAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT  
GGGGTGCTCTTCCTGGCCTCTGCTTCTGGATCCTCCCCACCCCTCTGCTCCTGGG  
GCCGCCCTTCTAGAGATCACTCAATAAACCTAAGAACCCCTATAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

696754-200506

## **FIGURE 18**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592
><subunit 1 of 1, 243 aa, 1 stop
><MW: 25298, pI: 6.44, NX(S/T): 0
MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHGSQGLPGRDGRDGRDGAPGAP
GEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP
FDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA
```

**Signal sequence.**

amino acids 1-15

**N-myristoylation sites.**

amino acids 11-17, 68-74, 216-222

**Cell attachment sequence.**

amino acids 77-80

## **FIGURE 19**

CTCTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG  
AAACAAGCCGGGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCAACAGACCCAT  
GCTGCATCCAGAGACCTCCCTGGCCGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTG  
GCACCACCTGGGAGAGGTGTGGCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC  
CTGAACAGGAAGGAGAGTTCTGCTCCTCCCTGCACAACCGCCTGCGCAGCTGGTCCA  
GCCCTGCGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCAACTGGCTCAAG  
CCAGGGCAGCCCTGTGGAATCCAACCCGAGCCTGGCATCCGGCTGTGGCGCACCTG  
CAAGTGGCTGGAACATGCAGCTGCTGCCCGGGCTTGGCGTCTTGTGAAGTGGTCAG  
CCTATGGTTGCAGAGGGCAGCGGTACAGCCACGCGCAGGAGAGTGTGCTCGAACGCCA  
CCTGCACCCACTACACGCAGCTCGTGGGCCACCTCAAGCCAGCTGGCTGTGGCGGCAC  
CTGTGCTCTGCAGGCCAGACAGCGATAGAACCTTGTCTGCTACTCCCCGGAGGCAA  
CTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAACGGTGCCTGGTGTGCTCTGCA  
CAGCCAGTGTCTCAGGCTGCTCAAAGCCTGGACCATGCAGGGGGCTGTGAGGTCCCC  
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTAACATCAGCACCTGCCACTG  
CCACTGTCCCCCTGGCTACACGGGAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTC  
ACGGCCGGTCCGGAGGAGGTGCTCGTGTGACATCGGCTACGGGGAGCCAG  
TGTGCCACCAAGGTGCATTTCCCTCACACCTGTGACCTGAGGATCGACGGAGACTGCTT  
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAGGCG  
GGGTGCTGGCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTGCCCTCTATCTGGCCGC  
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTCTGGATGGGCT  
CACCTACAAGACGCCAAGGACTCCTCCGCTGGGCCACAGGGAGCACCAGGCCTCACCA  
GTTTGCCCTTGGCAGCCTGACAACCACGGCTGGTGTGGCTGAGTGCTGCCATGGGTTT  
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCACTGGAAACGACCAGCGCTGCAAAAC  
CCGAAACCGTTACATCTGCCAGTTGCCAGGAGCACATCTCCGGTGGGCCAGGGCCT  
CGAGGCCTGACCACATGGCTCCCTGCCTGCCCTGGAGCACCGGCTCTGCTTACCTGTCTG  
CCACCTGTCTGGAACAAGGGCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGA  
CCTTGACAATGCCAGAAGTTGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG  
AGTGTAGAAGAAGCTGGGCCCTCGCCTGCTTTGATTGGAAAGATGGGCTTCATTAGA  
TGGCGAAGGAGAGGACACCGCCAGTGGTCAAAAAGGCTGCTCTTCCACCTGGCCAGAC  
CCTGTGGGCAGCGGAGCTCCCTGTGGCATGAACCCACGGGTATTAAATTATGAATCAG  
CTGAAAAAAAAAAA

090911-200800

## **FIGURE 20**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176  
<subunit 1 of 1, 455 aa, 1 stop  
<MW: 50478, pI: 8.44, NX(S/T): 2  
MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQQAPMAGALNRKESFLLSLHNRLRSWV  
QPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV  
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCRHLCAGQTAIEAFVCAYSPGG  
NWEVNGKTIIPYKKGAWSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSQNHGRLNISTCH  
CHCPCPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDC  
FMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLTTNEVTDSDFETRNFWIG  
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCK  
TRNRYICQFAQEHIISRWGPGS

**Signal sequence.**  
amino acids 1-26

**Transmembrane domain.**  
amino acids 110-124

**N-glycosylation sites.**  
amino acids 144-148, 243-247

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 45-49

**N-myristoylation sites.**  
amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,  
288-294, 331-337, 398-404

**Prokaryotic membrane lipoprotein lipid attachment site.**  
amino acids 204-215

**EGF-like domain cysteine pattern signature.**  
amino acids 249-261, 280-292

**C-type lectin domain signature.**  
amino acids 417-442

## FIGURE 21

CGGACGCGTGGCTGGCGCTGCAAAGCGTGTCCGCCGGTCCCCGAGCGTCCCGGCCCT  
CGCCCCGCC**ATG**CTCTGCTGCTGGGCTGTGCCTGGGCTGTCCCTGTGTGGGTGCGCA  
GGAAGAGGCCAGAGCTGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCGAGGCAAG  
TCAGACTGTTGCAAGAGCTGAAAACAAACCTTGATGACAGAAATTCTCAGTGAAGTCTACC  
ATCATTCCCGTTATGCCTCACTACGGTTCTGCAGAATGCTGAACAGAGCTCTGAAGA  
CCAGGACATTGAGTTCCAGATGCAGATTCCAGCTGCAGCTTCATCACCAACTTCACTATGC  
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGTAGG  
GTAAAAGAGAAAAGGAATAAAACACAGAAGAAAATGGAGAGAAGGGACTGAAATATTAG  
AGCTTCTGCAGTGATTCCCAGCAAGGACAAGCGCCTTTCTGAGTTATGAGGAGCTC  
TGCAGAGGCCCTGGCAAGTACGAGCACAGCATCAGCGTGCAGGCCAGCAGCTGTCGG  
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGATCCCTGGAGGTGCTGCC  
GCTTCACAACAGCAGGCAGAGGGCAGTGGCGGGAAAGATGATTCTGGCCTCCCCAT  
CTACTGTCATTAACCAAAATGAAACATTGCCAACATAATTAAACCTACTGTAGTACAA  
CAAGCCAGGATTGCCAGAATGGAATTGGAGACTTTATCATTAGATATGACGTCAATAG  
AGAACAGAGCATTGGGACATCCAGGTTCTAAATGGCTATTGTGACTACTTGCTCCTA  
AAGACCTTCCTCTTACCAAGAATGTGGTATTGTGCTTGACAGCAGTGCTCTATGGTG  
GGAACCAAACCTCCGGCAGACCAAGGATGCCCTCTCACAATTCTCCATGACCTCCGACCCCA  
GGACCGTTTCAGTATCATTGGATTTCACCGGATCAAAGTATGGAAGGACCACTTGATAT  
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGTACATTCAACATATGTCAACCACGTGGA  
GGCACAGACATCAACGGGCCCTGCAGAGGGCATTAGGCTCTCAACAAGTACGTGGCCCA  
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTTGACGGATGGGAAGGCCACGG  
TCGGGGAGACGCACACCCCAAGATCCTCAACAAACACCCGAGAGGCCGGAGGCCAAGTC  
TGCATCTTCACCATTGGCATGGCAACGACGTGGACTTCAGGCTGCTGGAGAAACTGTCGCT  
GGAGAACTGTGGCCTCACACGGCGGTGACGAGGAGGAGCAGCAGGCTCGCAGCTCATCG  
GGTTCTACGATGAAATCAGGACCCGCTCTCTGACATCCGCATCGATTATCCCCCAGC  
TCAGTGGTGCAGGCCACCAAGACCCCTGTTCCCAACTACTTCAACGGCTGGAGATCATCAT  
TGCAGGGAAAGCTGGTGACAGGAAGCTGGATCACCTGCACGTGGAGGTCACGCCAGCAACA  
GTAAGAAATTCATCCTGAAGACAGATGTGCCTGTGGCCTCAAGAAGGAGGGAAAGAT  
GTCACAGGAAGCCCCAGGCCTGGAGGCGATGGAGAGGGGACACCAACCACATGAGCGTCT  
CTGGAGCTACCTCACCAAAAGGAGCTGCTGAGCTCTGGCTGCAAAGTACGATGAGCTACCGCTCTCACTCCC  
AGAAGGAGCGGCTGGCGAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTCTCACTCCC  
TTCACCTCCATGAAGCTGAGGGGCCGGTCCCACGCATGGATGGCCTGGAGGAGGCCACGG  
CATGTCGGCTGCCATGGACCCGAACCGGGTGTGCAGAGCGTGCAGGGAGCTGGCACCGCAGC  
CAGGACCTTGCTCAAGAAGCCAAACTCCGTCAAAAAAAACAAACAAACAAAAAAGA  
CATGGGAGAGATGGTGTGTTCTCCACCACTGGGATACGAT**G**AGAAGATGGCCACCT  
GCAAGCCAGGAAGACGCCCTCACCAGACACCACATGCTGCTGGCACCTGATCTGGACCTC  
CCAGCCTCCAGAACTGTGAGAAATAATGTGTTAGCTAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 22**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192  
<subunit 1 of 1, 694 aa, 1 stop  
<MW: 77400, pI: 9.54, NX(S/T): 6  
MLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLLQRLKTKPLMTEFSVKSTIIS  
RYAFTTVSCRMLNRASEDQDIEFQMQIPAAAFITNFTMLIGDKVYQGEITEREKSGDRVKE  
KRNKTTTEENGKTEIFRASAVIPSVDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS  
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDEDSGPPPSTVINQNETFANIIFKPTVVQQAR  
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFVLDSSASMVGT  
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVWKDHLISVTPDSIRDGKVIHHMSPTGGTD  
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNNTREAARGQVCIF  
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV  
QATKTLFPNYFNGSEIIIAGKLVDRKLDHLHVEVTASNSKKFIILKTDVPVRPQKAGKDVTG  
SPRPGGDGECDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS  
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKQNKTKRHGR  
DGVFPLHHLGIR

**Signal sequence.**

amino acids 1-14

**N-glycosylation sites.**

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

**Glycosaminoglycan attachment sites.**

amino acids 213-217, 391-395

**N-myristylation sites.**

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

## **FIGURE 23**

CGGACGCGTGGGTGCCGACATGGCGAGTGTAGTGCTGCCAGCGGATCCCAGTGTGCGGC  
GGCAGCGCGCGCGCGCGCTCCCGGGCTCCGGCTTGCTGCTCTTCTCCGCCGCG  
CACTGATCCCCACAGGTGATGGGCAGAATCTGTTACGAAAGACGTGACAGTGATCGAGGGA  
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTCACTGAA  
TCCCAACAGGCAGACCATTATTCAGGGACTTCAGGCCTTGAAGGACAGCAGGTTCACT  
TGCTGAATTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTCTGATGAA  
GGAAGATACTTTGCCAGCTCTACCGATCCCCACAGGAAAGTTACACCACCATCAGT  
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG  
AGATTGAAGTCAACTGCACTGCTATGCCAGCAAGCCAGCCACGACTATCAGGTGGTCAAA  
GGGAACACAGAGCTAAAGGCAAATCGGAGGTGGAAGAGTGTCAGACATGTACACTGTGAC  
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGTCCAGTGATCTGCCAGGTGG  
AGCACCCTGCGGTCACTGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT  
CAAGTGCACATTGAGACTTACCTCTACAAGGCTAACCGGGAAAGGGACGCGCTTGA  
GTTAACATGTGAAGCCATCGGAAGCCCCAGCCTGTGATGGTAACGGTGAGAGTCGATG  
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCAACCTGTTCATCAATAACCTAAACAAA  
ACAGATAATGGTACATACCGCTGTGAAGCTCAAACATAGGGAAAGCTCACTCGGATTA  
TATGCTGTATGTATACGATCCCCACAACATCCCTCCTCCCACAACAACCACCA  
CCACCACCACCACCAACCACCATCCTTACCATCATCACAGATTCCGAGCAGGTGAAGAAGGC  
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTGGCGGTGGTGGTGGTGCAT  
GCTGTGCTTGCTCATCATTCTGGGCGCTATTTGCCAGACATAAGGTACATACTTCACTC  
ATGAAGCCAAAGGAGCCGATGACGCAGCAGCAGACACAGCTATAATCAATGCAGAAGGA  
GGACAGAACAACTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTGTTCAAT  
GAGGTGTCCAATGGCCCTATTAGATGATAAAGAGACAGTGATATTGG

## **FIGURE 24**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518  
<subunit 1 of 1, 440 aa, 1 stop  
<MW: 48240, pI: 4.93, NX(S/T): 7  
MASVVLPSGSQCAAAAAAAPPGLLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC  
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQL  
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTTELKG  
KSEVEEWSDMYTVTSQMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT  
YPLQGLTREGDALELTCEAIGKPQPMVTWVRVDEMPQHAVLSGPNLFINNLNKTDNGTYR  
CEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTILTIITDSRAGEEGSIRAVDH  
AVIGGVVAVVVFAMLCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE  
KKEYFI

**Signal sequence.**

amino acids 1-36

**Transmembrane domain.**

amino acids 372-393

**N-glycosylation sites.**

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,  
430-434

**Tyrosine kinase phosphorylation sites.**

amino acids 233-240, 319-328

**N-myristoylation sites.**

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,  
411-417, 427-433, 428-432

200300-2544466.0

## FIGURE 25

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTGGGCCCGA  
CCCGCCAGGAAAGACTGAGGCCGCGCCTGCCCGCCGGCTCCCTGCGCCGCCGCCCTC  
CCGGGACAGAAGATGTGCTCCAGGGTCCAGGCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT  
GGGGCCTGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGACGCCACAGACAGTCTTCT  
GCACTGCCGCCAGGGACCACGGTCCCCGAGACGTGCCACCCGACACGGTGGGCTGTAC  
GTCTTGAGAACGGCATCACCATGCTGACGCAAGCAGCTTGCAGGCCCTGCGCCGGCTGCA  
GCTCCTGGACCTGTCACAGAACCGAGATGCCAGCCTGCGCCTGCCCGCTGCTGCTGG  
ACCTCAGGCCAACACAGCCTGCCCTGGGCCATGGACACTGCCAACGTGGAG  
GCGCTGCGGCTGGCTGGTCTGGGCTGCAGCAGCTGGACGAGGGCTTCAAGCCGTTGCG  
CAACCTCACGACCTGGATGTGTCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG  
GCCTCCGGGGCCTGACGCCCTGCCGGCTGCCGGAACACCCGATTGCCAGCTGCC  
GAGGACCTGCCGGCCTGGCTGCCCTGCAAGGAGCTGGATGTGAGCAACCTAACGCTGCAGGC  
CCTGCCCTGGCACCTCTGGGCCCTTCCCCGCCCTGCCAGCTGCCAAC  
CCTTCAACTGCGTGTGCCCTGAGCTGGTTGGCCCTGGGTGCGAGAGGCCACGTACA  
CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCACCAAGAACGCTGGCCGGCTGCTCCT  
GGAGCTTGATACGCCACTTGGCTGCCAGCCACCACACCAGCCACAGTGCCACCCA  
CGAGGCCGTGGTGCGGGAGCCCACAGCCTGTCTTAGCTGGCTCCTACCTGGCTTAGC  
CCCACAGCGCCGCCACTGAGGCCAGGCCCTCCACTGCCAACCGACTGTAGGGCC  
TGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCCAATGGGGCACATGCCACCTGG  
GGACACGGCACCACTGGCGTGTGGCCCGAAGGCTTACGGGCTGTACTGTGAGAGC  
CAGATGGGCAGGGACACGCCAGCCCTACACCAGTCAGCCGAGGCCACCACGGTCC  
GACCCCTGGCATCGAGCCGTGAGCCCCACCTCCCTGCCGTGGGCTGCAGCGCTACCTCC  
AGGGGAGCTCGTGCAGCTCAGGAGCCTCCGTCTCACCTATGCAACCTATGGCCCTGAT  
AAGCGGCTGGTGACGCTGCGACTGCCCTGCCCTCGCTGAGTACACGGTCAACCAGCTGCG  
GCCCAACGCCACTTACTCCGTCTGTGTCATGCCCTTGGGCCCCGGGGTGCAGGGAGGGCG  
AGGAGGCCTGCCGGAGGCCATACACCCCAAGCCGTCCACTCCAACCACGCCAGTCACC  
CAGGCCCGCAGGGCAACCTGCCCTCCATTGCCCGCCCTGGCGGGTCTGGC  
CGCGCTGGCTGCCGTGGGGCAGCCTACTGTGTGCCGGGGGGCCATGGCAGCAGCG  
CTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGGCCCTGGAACTGGAGGGAGTGAAGGTC  
CCCTGGAGCCAGGCCAGGCAAGGAAACAGAGGGCGGTGGAGAGGCCCTGCCAGGGCTGA  
GTGTGAGGTGCCACTCATGGCTTCCCAGGGCTGCCCTCCAGTCACCCCTCCACGCAAAGC  
CCTACATTAACCAGAGAGAGACAGGGCAGCTGGGCCGGCTCTAGCCAGTGAGATGGC  
CAGCCCCCTCTGCTGCCACACCACGTAAGTTCTCAGTCCAAACCTGGGATGTGCGAGA  
CAGGGCTGTGTGACCACAGCTGGCCCTGTTCCCTCTGGACCTCGGTCTCTCATCTGTGAG  
ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCTATGAGGACAGTGT  
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGCACGGCGGGCCCTGCCATGTGCTGTAAC  
GCATGCCCTGGCCCTGCTGGCTCTCCACTCCAGGCAGGCCCTGGGGCCAGTGAAGGAAG  
CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGACTCTAGTCTGGCCCGAGG  
AAGCGAAGGAACAAAGAAACTGGAAAGGAAGATGCTTAGGAACATGTTGCTTTTAA  
AATATATATATTTATAAGAGATCCTTCCCATTATTCTGGGAAGATGTTTCAAAC  
AGAGACAAGGACTTGGTTTGTAAAGACAAACGATGATGAAGGCCCTTGTAAAGAAAAA  
ATAAAAAAAAAA

## **FIGURE 26**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pi: 7.24, NX(S/T): 3

MCSRVPLLLPLLLLALGPGVQGCPGQCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFEN  
GITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILD TANVEALRL  
AGLGLQQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA  
GLAALQELDVSNLSQLPGDLSGLFPRLRLLAAARNPNCVCPLSWFGPWVRESHVTLASP  
EETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSLAPTWLSPTAP  
ATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQ  
GTRPSPTPVTPRPPRSLTGIEPVSPSTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLV  
TLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE  
GNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAQDKGQVGPAGPLELEGVKVPLEP  
GPKATEGGGEALPSGSECEVPLMGMFPGPGLQSPLHAKPYI

**Signal sequence.**

amino acids 1-23

**Transmembrane domain.**

amino acids 501-522

**N-glycosylation sites.**

amino acids 198-202, 425-429, 453-457

**Tyrosine kinase phosphorylation site.**

amino acids 262-270

**N-myristoylation sites.**

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**EGF-like domain cysteine pattern signature.**

amino acids 355-367

**Leucine zipper pattern.**

amino acids 122-144, 194-216

## **FIGURE 27**

GGCACTAGGACAACCTTCTTCCCTCTGCACCACTGCCGTACCCCTAACCGCCCCGCCACC  
TCCTTGCTACCCACTCTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTC**ATGCCAGCCTC**  
ATCTCCTTCTTGCTAGCCCCAAAGGGCCTCCAGGCAACATGGGGGCCAGTCAGAGAGC  
CGGCACTCTCAGTTGCCCTCTGGTGAGTTGGGGGCAGCTCTGGGGCCGTGGCTTGCC  
ATGGCTCTGCTGACCCAAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA  
GGGGACAGGAGGCCCCCTCCAGAATGGGAAGGGTATCCCTGGCAGAGTCTCCGGAGCAGA  
GTTCCGATGCCCTGGAAGCCTGGAGAATGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC  
ACCCAAAAACAGAAGAAGCAGCACTCTGTCCTGCACCTGGTCCCATTAAACGCCACCTCCAA  
GGATGACTCCGATGTGACAGAGGTATGTGGCAACCAGCTCTAGGCGTGGAGAGGCCTAC  
AGGCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTATCTGCTGTATAGCCAGGTC  
CTGTTCAAGACGTGACTTCACCATGGTCAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA  
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGGACCAGGGCTACAACAGCT  
GCTATAGCGCAGGTGTCTCCATTACACCAAGGGATATTCTGAGTGTCTAATTCCCCGG  
GCAAGGGCGAAACTTAACCTCTCCACATGGAACCTCCTGGGTTGTGAAACTGT**GATT**  
GTGTTATAAAAGTGGCTCCAGCTTGGAAAGACCAGGGTGGTACATACTGGAGACAGCCAA  
GAGCTGAGTATAAAGGAGAGGAATGTGCAGGAACAGAGGCATCTCCTGGGTTGGCTC  
CCCGTTCTCCTACTTCCCTTTCTTCAATTCCACCCCTAGACTTGTGATTACGGATATCTG  
CTTCTGTTCCCCATGGAGCTCCG

## **FIGURE 28**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27433, pi: 9.85, NX(S/T): 2
MPASSPFL LAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV
SRLQGTGGPSQN GEGYPWQSLPEQSSDALEAWENGERSRKRAVL TQKQKKQHSVLHLVPIN
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREG
QGRQETLFRCIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVII PRARAKLNLSPHGTFLGFVKL
```

**Signal sequence.**

amino acids 1-40

**N-glycosylation site.**

amino acids 124-128

**Tyrosine kinase phosphorylation site.**

amino acids 156-164

**N-myristoylation site.**

amino acids 36-42, 40-46, 179-185, 242-248

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 34-45

100000 200000 300000 400000 500000

## **FIGURE 29**

CACTTTCTCCCTCTTCCTTACTTCGAGAAACCGCGCTCCGCTCTGGTCGCAGAGAC  
CTCGGAGACCGCGCCGGGAGACGGAGGTGCTGTGGGTGGGGGACCTGTGGCTGCTCGTA  
CCGCCCCCCCACCCCTCCTCTGCACTGCCGTCTCGGAAGACCTTTCCCCCTGCTCTGTT  
TCCTTCACCGAGTCTGTGCATGCCCGGACCTGGCCGGAGGAGGCTGGCCGGCGGGAGA  
TGCTCTAGGGCGCGCGGGAGGAGCAGGACGGAGGGCCCGCAGGAAG**ATGGC**  
TCCCCTGGACAGGGACTCTGCTGGCTACTGCCTGCTCCTGCCTTGCCCTGGCCTGGT  
CCTGAGTCGTGTGCCCATGTCCAGGGGAACAGCAGGAGTGGAGGGACTGAGGAGCTGC  
CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAAACATGAAAATACAGGCCAGTCAG  
GACCAGGGCTCCCTGCTTCCGGTCTGCCTGCTGTGACCCGGTACCTCCATGTACCC  
GGCAGCCGTGCCAGATCAACATCACTATCTGAAAGGGAGAAGGGTACCGCCAG  
ATCGAGGCCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGCCAGGGCACACTGGA  
CCAAAGGGCAGAAGGGCTCCATGGGGCCCTGGGGAGCAGTGCAGAGGCCACTACGCC  
CTTTCTGGTGGGCCGGAGAACGCCATGCACAGCAACACTACTACAGACGGTATCTCG  
ACACGGAGTCGTGAACCTCTACGACCACTCAACATGTTCACCGCAAGTTCTACTGCTAC  
GTGCCCGGCCTCTACTTCTCAGCCTCAACGTGCACACCTGGAACCAGAAGGAGACCTACCT  
GCACATCATGAAGAACGAGGGAGGAGGTGGTATCTGTTCGCGCAGGTGGCGACCGCAGCA  
TCATGCAAAGCCAGGCCTGATGCTGGAGCTGCAGAGCAGGACCAAGGTGTGGTACGCC  
TACAAGGGCGAACGTGAGAACGCCATCTCAGCGAGGAGCTGGACACCTACATCAC  
TGGCTACCTGGTCAAGCACGCCACCGAGCC**TAG**CTGGCCGCCACCTCCTTCC  
ACCTTCACCCCTGCGCTGTGCTGACCCACCGCCTTCCCCGATCCCTGGACTCCGACTC  
CCTGGCTTGGCATTCACTGAGACGCCCTGCACACACAGAAAGCCAAGCGATCGGTGCTCC  
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAAGGGCGGGCACCG  
GAGAACCCCTCTGGGACCTCCGCGGCCCTCTGCACACATCCTCAAGTGACCCGCACGG  
GAGACGCGGGTGGCGCAGGGCGTCCCAGGGTGCAGCAGGCTCCAGTCCTGGAAATA  
ATTAGGCAAATTCTAAAGGTCTAAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG  
TTGTTATTTTGTCTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGGCTTTCAAGTGAG  
ACTCTGCTTAAGAGAACGATCCAAGTTAAAGCTCTGGGTAGGGAGGGCCGGGGCAGG  
AAACTACCTCTGGCTTAATTCTTTAAGCCACGTAGGAACCTTCTGAGGAGATGGGAC  
CTGACATCCCTGTGGCCTGCCCCAAGGGCTCTGCTGGTCTTCTGAGTCACAGCTGCAGGT  
GATGGGGCTGGGCCCCAGGCAGCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC  
TCCAGGGTGGTAGAACGAGCCGAAGGGCTCTGACAGTGGCAGGGACCCCTGGTCCCC  
GGCCTGCAGATGTTCTATGAGGGCAGAGCTCCTGGTACATCCATGTGTGGCTCTGCTCC  
ACCCCTGTGCCACCCAGAGCCCTGGGGGTGGCTCCATGCCTGCCACCTGGCATCGGCT  
TTCTGTGCCGCCCTCCCACACAAATCAGCCCCAGAAGGCCCGGGCCTGGCTCTGTTTT  
TATAAAACACCTCAAGCAGCACTGCAGTCCTCCATCTCCTCGTGGCTAACGATCACCGCTT  
CCACGTGTGTTGTGGTGGCAGCAAGGCTGATCCAGACCCCTCTGCCCTTACTGCC  
CATCCAGGCCTCTGACCACTGAGGAGGGCTTTCTAGGCTTCAGAGCAGGGAGAG  
CTGGAAAGGGCTAGAAAGCTCCGCTTGTCTGTTCTCAGGCTCCTGTGAGCCTCAGTCCTG  
AGACCAAGAGTCAAGAGGAAGTACACGTCCAATCACCGTGTCAAGGATTCACTCTCAGGAGC  
TGGGTGGCAGGAGAGGAATAGCCCTGTGGCAATTGCAGGACCAAGCTGGAGCAGGGTGC  
GTGTCTCCACGGTGTCTGCCCTGCCATGCCACCCAGACTCTGATCTCCAGGAACCC  
ATAGCCCTCTCCACCTCACCCATGTTGATGCCAGGGTCACTCTGCTACCCGCTGGGCC  
CCAAACCCCCGCTGCCCTCTTCCCTCCCCCATCCCCCACCTGGTTTGACTAATCCTGC  
TTCCCTCTCTGGGCTGGCTGCCGGATCTGGGTCCTAACGCTCCCTCTTTAAAGAACTT  
CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGCGTGCCTGGGAAGCAGAGGCCACACTC  
GCTGCTTAAGCTCCCCAGCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTCAA

## **FIGURE 30**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSGRKPKMHSNYYQTVIFDTEFVNLYDHFNMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEVVILFAQVGDRSIMQSQSLMELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP
```

**Signal sequence.**

amino acids 1-25

**N-glycosylation site.**

amino acids 93-97

**N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

**Amidation site.**

amino acids 150-154

**Cell attachment sequence.**

amino acids 104-107

2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010

## **FIGURE 31**

GC GGAGCATCCGCTCGGGTCTCGCCGAGACCCCCCGCGGGATTGCCGGCTTCCCGGG  
GCGCAGAGCTGCTCTCGCACCTGGATGGCAGCAGGGCGCCGGGTCTCTGACGCCA  
GAGAGAAATCTCATCATCTGTGCAGCCTCTTAAAGCAAACTAAGACCAGAGGGAGGATTAT  
CCTTGACCTTGAAGACAAAACACTAAACTGAAATTAAAATGTTCTCGGGGAGAAGGGAG  
CTTGACTTACACTTGGTAATAATTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAATT  
GCCTCAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTCTAAGGGAAATC  
AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAAATTCTGCTGTTCAAC  
AAAAAACATATCAGGGACAAAGCATGTAACCTGATGATCTCGACACTCGAAAAACAGCTA  
GACAACCCAACTGCTACCTATTCTGTCCCAACGAGGAAGCCTGTCATTGAAACCAGCA  
AAAGGACTTATGAGTTACAGGATAATTACAGATTTCATCTTGCACAGAAATTGCAAG  
CCAAGAGTTACCCCAGGAAGATTCTCTTACATGCCAATTTCACAAGCAGTCACCCCC  
TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTCT  
CAGAAGTTGGATCCTCAGATCACCTGGAGAAACTATTAAAGATGGATGAAGCAAGTGC  
GCTCCTGCTTATAAGGAAAAGGCCATTCTCAGAGTTCACAAATTTCCTCTGATCAAGAAA  
TAGCTCATCTGCTGCCTGAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCA  
CATACCACCTCGGCTACTCCAAAGCCCCACCCTCTACCCACCAATGCTTCAGTACACC  
TTCTGGGACTTCCCAGGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACACTGTC  
AGCCTCCCACGACCCCTATTCTACAGTTTACACGGGCTGGCTACACTCCAAGCAATG  
GCTACAACAGCAGTTCTGACTACCACCTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA  
AACCATAACGTTTACAGAAATCTCAAACCTAACCTTGAACACAGGGAATGTGTATAACCCTA  
CTGCACTTCTATGTCAAATGTGGAGTCTCCACTATGAATAAAACTGCTCCTGGGAAGGT  
AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTCCAGAAAATCAGTACGGCCTTCC  
ATTGAAAATGGCTTCTTATCGGGTCCCTGCTTTGGTGTCTGGTCTGGTGTAGGCC  
TCGTCTCCTGGTAGAATCCTTCAGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT  
TATTGATCAATGGATCTATGTGGACATCTAAGGATGGAACCTGGTGTCTCTTAATTCTT  
TAGTAACCAGAAGCCAAATGCAATGAGTTCTGCTGACTGCTAGTCTTAGCAGGAGGTTG  
TATTGAAAGACAGGAAAATGCCCTCTGCTTCTTCTTGGAGACAGAGTCTT  
GCTCTGTTGCCAGGGCTGGAGTGCAGTAGCAGGATCTGGCTCTCACCGAACCTCCGTCTC  
CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCTAACGATCTGGGATTACAGGATGTGCCA  
CCACACCTGGGTGATTGGTATTAGTAGAGACGGGTTTACCATGTTGGTCAGGCTG  
GTCTCAAACCTCTGACCTAGTGTACCTGGCAGGCTCCAAAGTGTCTGGGATTACAGG  
CATGAGCCACACAGCTGGCCCCCTCTGTTTATGTTGGTTTGAGAAGGAATGAAGTG  
GGAACCAAATTAGGTAATTGGTAATCTGTCTAAATATTAGCTAAAACAAAGCTCT  
ATGTAAGTAATAAAAGTATAATTGCCATATAAAATTCAAACGGCTTTATGCAA  
GAAACAGGTTAGGACATCTAGGTTCCAATTCACTCACATTCTGGTCCAGATAAAATCAAC  
TGTTTATATCAATTCTAATGGATTGCTTCTTTATATGGATTCTTAAACTTATT  
CCAGATGTAGTTCTCCAATTAAATATTGAATAAAATCTTTGTTACTCAA

## **FIGURE 32**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVII CFLTLRLSASQNCLKSLEDVVIDIQSSL SKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDY SKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENV SALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTA SWEGREASPGSSSQGSV
PENOYGLPFEKWLLIGSLLFGVLFVIGLVLLGRILSESLRRKRYSRLDYILINGIYVDI
```

### Signal sequence.

## amino acids 1-25

#### Transmembrane domain.

amino acids 384-405

### N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

### Tyrosine kinase phosphorylation site.

amino acids 50-57

### N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

## **FIGURE 33**

CGGGCACCTGGAAGATGCGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTTCGTGGCTTC  
GCCTCCTTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT  
GTCCAGTGCTGCCTATAGCATCCGCAGCATGGGGAGAGGCCCTGTCCTCAAAGCTCCAGTCC  
CCAAAAGGCAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA  
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTGAGGATAACCTACTTATGGG  
AGAACAGCTGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACGGGA  
ATGTGACAGCAACACGATGTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG  
TTTATTCAAGAGTGCCTGCCAAAATCCCTGCTCTTCATGGTACCTATGACGACGGAAGCAC  
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAAGTAAAGAAATCAGGAACA  
TGAAATTCAAGGTCTAGCTGGTATTATTGCAGCAAAAGGCTTGGAACTCCCTCCGAAATT  
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACACAGATATTCTGGCTGGCCTGCAGA  
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTGACACTGCAGGGCCTGAGTAAAT  
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAACATCTTATTTCTAAATCCAACA  
GCCCATATTGATGAGTATTTGGGTTGTTGAAACCAATGAACATTGCTAGTTGTATCA  
AATCTTGGTACGCAGTATTTTATACCAGTATTTATGTAAGTGAAGATGTCAATTAGCAGGA  
AACTAAAATGAATGGAATTCTAAAAAAAAAA

## **FIGURE 34**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777

><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

MRPLAGGLLKVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK  
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT  
RCFDMDYEGDNGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS  
SWVFTAAGLELPSEIOREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

### Signal sequence.

amino acids 1-20

### N-glycosylation sites.

amino acids 120-124, 208-212

#### Glycosaminoglycan attachment site.

amino acids 80-84

### N-myristoylation sites.

amino acids 81-87, 108-114, 119-125